features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the inventions embodied therein herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention.

The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein.

Other embodiments are within the following claims. In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group.

CLAIMS

We claim:

1. An expressed sequence tag ("EST"), wherein said EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies said cell as a developmentally competent cell.

2. An expressed sequence tag ("EST"), wherein said EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies said cell as a developmentally incompetent cell.

3. A gene expression database comprising:

two or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of two or more genes, the expression of which, or their complementary sequences, in a cell identifies said cell as a developmentally competent cell.

4. A gene expression database comprising:

two or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of two or more genes, the expression of which, or their complementary sequences, in a cell identifies said cell as a developmentally incompetent cell.

5. A gene expression database comprising:

one or more first expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of one or more genes, the expression of which, or their complementary sequences, in a cell identifies said cell as a developmentally competent cell; and

one or more second expressed sequence tags, wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of one or more genes, the expression of which, or their complementary sequences, in a cell identifies said cell as a developmentally incompetent cell.

6. A gene expression database according to any one of claims 3, 4, or 5, comprising at least 10 different ESTs.

7. A gene expression database according to any one of claims 3, 4, or 5, comprising at least 100 different ESTs.

8. A gene expression database according to any one of claims 3, 4, or 5, comprising at least 1000 different ESTs.

9. A gene expression database according to any one of claims 3, 4, or 5, comprising at least 5000 different ESTs.

10. A gene expression database according to any one of claims 3, 4, or 5, comprising at least 10,000 different ESTs.

11. A gene expression database according to any one of claims 3, 4, or 5, wherein ESTs are obtained from the same species as said cell.

12. A gene expression database according to any one of claims 3, 4, or 5, wherein said cell is a mammalian cell.

13. A gene expression database according to claim 12, wherein said mammalian cell is an ungulate cell.

14. A gene expression database according to claim 13, wherein said ungulate cell is a bovine cell.

15. A method of identifying an expressed sequence tag ("EST"), wherein said EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, identifies said cell as a developmentally competent cell, the method comprising:

comparing one or more first nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally competent nuclear donor cell to one or more second nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally incompetent nuclear donor cell; and

identifying a nucleic acid molecule present in said first nucleic acid molecules that is not present at a detectable level in said second nucleic acid molecules.

16. A method of identifying an expressed sequence tag ("EST"), wherein said EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, identifies said cell as a developmentally incompetent cell, the method comprising:

comparing one or more first nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally competent nuclear donor cell to one or more second nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally incompetent nuclear donor cell; and

identifying a nucleic acid molecule present in said second nucleic acid molecules that is not present at a detectable level in said first nucleic acid molecules.

17. A method of preparing a gene expression database comprising two or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of two or more genes, the expression of which, or their complementary sequences, identifies said cell as a developmentally competent cell, the method comprising:

comparing a first plurality of nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally competent nuclear donor cell to a second plurality of nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally incompetent nuclear donor cell;

identifying two or more nucleic acid molecules present in said first plurality of nucleic acid molecules that are not present at a detectable level in said second plurality of nucleic acid molecules to provide two or more identified nucleic acid molecules; and

combining said identified nucleic acid molecules in a gene expression database.

18. A method of preparing a gene expression database comprising two or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of two or more genes, the expression of which, or their complementary sequences, identifies said cell as a developmentally incompetent cell, the method comprising:

comparing a first plurality of nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally competent nuclear

donor cell to a second plurality of nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally incompetent nuclear donor cell;

identifying two or more nucleic acid molecules present in said second plurality of nucleic acid molecules that are not present at a detectable level in said first plurality of nucleic acid molecules to provide two or more identified nucleic acid molecules; and

combining said identified nucleic acid molecules in a gene expression database.

19. A method of preparing a gene expression database comprising one or more first expressed sequence tags ("ESTs"), wherein said EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, identifies said cell as a developmentally competent cell, and one or more second expressed sequence tags, the expression of which in a cell identifies said cell as a developmentally incompetent cell, the method comprising:

comparing a first plurality of nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally competent nuclear donor cell to a second plurality of nucleic acid molecules obtained from one or more embryos produced by nuclear transfer using a developmentally incompetent nuclear donor cell;

identifying one or more nucleic acid molecules present in said first plurality of nucleic acid molecules that are not present at a detectable level in said second plurality of nucleic acid molecules and identifying one or more nucleic acid molecules present in said second plurality of nucleic acid molecules that are not present at a detectable level in said first plurality of nucleic acid molecules to provide two or more identified nucleic acid molecules; and

combining said identified nucleic acid molecules in a gene expression database.

20. A method according to any one of claims 17, 18, or 19, wherein said comparing step comprises comparing said first and/or said second plurality of nucleic acid molecules to a reference nucleic acid library obtained from an animal of the same species as said developmentally competent or said developmentally incompetent nuclear donor cell.

21. A method of producing one or more animals by nuclear transfer procedures using a competent nuclear donor cell, the method comprising:

(a) performing one or more nuclear transfer procedures to provide one or more nuclear transfer embryos;

(b) culturing each of said nuclear transfer embryos to provide one or more embryos comprising at least two cells;

(c) separating at least one cell from each of said embryos to provide one or more isolated embryonic cell populations;

(d) determining the developmental competence of each of said embryonic cell populations by comparing one or more nucleic acid molecules obtained from each of said embryonic cell populations to a gene expression database, whereby said comparison identifies those embryos resulting from nuclear transfer of a developmentally competent nuclear donor cell; and

(e) implanting embryos resulting from nuclear transfer of a developmentally competent nuclear donor cell into one or more recipient females for development into said one or more animals.

22. A method according to claim 21, wherein said one or more animals are one or more mammalian animals.

23. A method according to claim 22, wherein said one or more mammalian animals are one or more bovine animals.

24. A method according to claim 21, wherein said nuclear transfer procedures comprise using a transgenic nuclear donor cell.

25. A method of identifying a developmentally competent nuclear donor cell line, the method comprising:

(a) separating one or more cells from a cell line to provide one or more separated cells;

(b) performing one or more nuclear transfer procedures using each of said separated cells to provide one or more nuclear transfer embryos; and

(c) determining the developmental competence of each of said nuclear transfer embryos by comparing a plurality of nucleic acid molecules obtained from each of said embryos to a gene expression database, whereby said comparison identifies those embryos resulting from nuclear transfer of a developmentally competent nuclear donor cell.

26. A method according to claim 25, wherein said method further comprises culturing said nuclear transfer embryos prior to determining the developmental competence of each of said nuclear transfer embryos.

27. A method according to claim 25, wherein said one or more animals are one or more mammalian animals.

28. A method according to claim 27, wherein said one or more mammalian animals are one or more bovine animals.

29. A method according to claim 25, wherein said nuclear donor cell line is a transgenic nuclear donor cell line.

30. A method of producing one or more embryos by nuclear transfer procedures using a competent nuclear donor cell, the method comprising:

(a) performing one or more nuclear transfer procedures to provide one or more nuclear transfer embryos;

(b) culturing each of said nuclear transfer embryos to provide one or more embryos comprising at least two cells;

(c) separating at least one cell from each of said embryos to provide one or more isolated embryonic cell populations; and

(d) determining the developmental competence of each of said embryonic cell populations by comparing one or more nucleic acid molecules obtained from each of said embryonic cell populations to a gene expression database, whereby said comparison identifies those embryos resulting from nuclear transfer of a developmentally competent nuclear donor cell.

31. A method to assess the effect of one or more changes in a nuclear transfer protocol, the method comprising:

(a) performing one or more nuclear transfer procedures according to a first nuclear transfer protocol to produce one or more first protocol nuclear transfer embryos;

(b) performing one or more nuclear transfer procedures according to a second nuclear transfer protocol comprising one or more changes to said first nuclear transfer protocol, to produce one or more second protocol nuclear transfer embryos;

(c) determining the developmental competence of each of said first protocol and second protocol nuclear transfer embryos by comparing a plurality of nucleic acid molecules obtained from each of said embryos to a gene expression database, whereby said comparison identifies those embryos; and

(d) assessing the effect of said one or more changes by comparing the developmental competence of said first protocol nuclear transfer embryos to the developmental competence of said second protocol nuclear transfer embryos.

32. A method according to claim 31, wherein said method further comprises culturing said first protocol nuclear transfer embryos and/or said second protocol nuclear transfer embryos prior to determining the developmental competence of each of said nuclear transfer embryos.

33. A method according to claim 31, wherein said nuclear transfer procedures comprise using a mammalian nuclear donor cells.

34. A method according to claim 33, wherein said mammalian nuclear donor cells are bovine nuclear donor cells.

35. A nucleic acid array comprising:

two or more different nucleic acid molecules, the expression of which in a cell identifies said cell as a developmentally competent cell, wherein each of said different nucleic acid molecules is affixed to a solid matrix.

36. A nucleic acid array comprising:

two or more different nucleic acid molecules, the expression of which in a cell identifies said cell as a developmentally incompetent cell, wherein each of said different nucleic acid molecules is affixed to a solid matrix.

37. A nucleic acid array comprising:

at least one nucleic acid molecule, the expression of which in a cell identifies said cell as a developmentally competent cell; and

at least one nucleic acid molecule, the expression of which in a cell identifies said cell as a developmentally incompetent cell,

wherein each of said different nucleic acid molecules is affixed to a solid matrix.

38. A nucleic acid array according to any one of claims 35, 36, or 37, wherein each different nucleic acid molecule is positioned at a different spatial location on said solid matrix.

39. A nucleic acid array according to any one of claims 35, 36, or 37, wherein said solid matrix comprises a material selected from the group consisting of polyacrylamide gel, agarose gel, nitrocellulose membrane, nylon membrane, glass, magnetic materials, magnetic beads, polymeric beads, or silicon.

40. A gene expression database comprising:

two or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of two or more genes, the expression of which, or their complementary sequences, in a stem cell identifies said stem cell as capable of committing to a specific cell lineage.

41. A gene expression database comprising:

two or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of two or more genes, the expression of which, or their complementary sequences, in a stem cell identifies said stem cell as incapable of committing to a specific cell lineage.

42. A gene expression database comprising:

at least one expressed sequence tag ("ESTs"), wherein said EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a stem cell identifies said stem cell as capable of committing to a specific cell lineage; and

at least one expressed sequence tag, wherein said EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a stem cell identifies said stem cell as incapable of committing to a specific cell lineage.

43. A method of preparing a gene expression database comprising two or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of two or more genes, the expression of which, or their complementary sequences, in a stem cell identifies said stem cell as capable of committing to a specific cell lineage, the method comprising:

comparing a first plurality of nucleic acid molecules obtained from one or more stem cells known to be capable of differentiation into a specific cell type to a second plurality of nucleic acid molecules obtained from one or more stem cells known to be incapable of differentiation into a specific cell type; and

identifying two or more nucleic acid molecules present in said first plurality of nucleic acid molecules that are not present at a detectable level in said second plurality of nucleic acid molecules.

44. A method of preparing a gene expression database comprising two or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of two or more genes, the expression of which, or their complementary sequences, in a stem cell identifies said stem cell as incapable of committing to a specific cell lineage, the method comprising:

comparing a first plurality of nucleic acid molecules obtained from one or more stem cells known to be capable of differentiation into a specific cell type to a second plurality of nucleic acid molecules obtained from one or more stem cells known to be incapable of differentiation into a specific cell type; and

identifying two or more nucleic acid molecules present in said second plurality of nucleic acid molecules that are not present at a detectable level in said first plurality of nucleic acid molecules.

45. A method of preparing a gene expression database comprising one or more expressed sequence tags ("ESTs"), wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of one or more genes, the expression of which, or their complementary sequences, in a stem cell identifies said stem cell as capable of committing to a specific cell lineage, and one or more expressed sequence tags, wherein said ESTs are isolated, enriched, or purified nucleic acid sequences representing all or part of one or more genes, the expression of which, or their complementary sequences, in a stem cell identifies said stem cell as incapable of committing to a specific cell lineage the method comprising:

comparing a first plurality of nucleic acid molecules obtained from one or more stem cells known to be capable of differentiation into a specific cell type to a second plurality of nucleic acid molecules obtained from one or more stem cells known to be incapable of differentiation into a specific cell type; and

identifying one or more nucleic acid molecules present in said first plurality of nucleic acid molecules that are not present at a detectable level in said second plurality of nucleic acid molecules, and identifying one or more nucleic acid molecules present in said second plurality of nucleic acid molecules that are not present at a detectable level in said first plurality of nucleic acid molecules.

46. A method of identifying one or more molecules that induce developmental competence in a cell line, the method comprising:

(a) contacting a developmentally incompetent cell line with one or more molecules to provide a treated cell line;

(b) separating one or more cells from said treated cell line to provide one or more separated cells;

(c) performing one or more nuclear transfer procedures using each of said separated cells to provide one or more nuclear transfer embryos; and

(d) determining the developmental competence of each of said nuclear transfer embryos by comparing a plurality of nucleic acid molecules obtained from each of said embryos to a gene expression database, whereby said comparison identifies those embryos resulting from nuclear transfer of a developmentally competent nuclear donor cell.

47. A method according to claim 46, wherein said cell line is selected from the group consisting of a cell line derived from cells isolated from an embryo arising from the union of two gametes in vitro or in vivo; an embryonic stem cell line; a cell line arising from inner cell mass cells isolated from of embryos; a cell line obtained from pre-blastocyst cells; a fetal cell line; a primordial germ cell line; a germ cell line, an embryonic germ cell line, a somatic cell line isolated from an animal; a cumulus cell line; an amniotic cell line; a fetal fibroblast cell line; a genital ridge cell line; a differentiated cell line; a lineage-specific cell line; and a totipotent cell line.

48. A method of inducing totipotence in a cell line, the method comprising:

(a) contacting said cell line with one or more molecules identified as inducing developmental incompetence in a cell line by the method of claim 46, whereby one or more cells of said cell line become developmentally competent.

49. A method of treating a disease in an animal by inducing totipotence in one or more cells of the animal, the method comprising:

(a) administering one or more molecules identified as inducing developmental competence in a cell line by the method of claim 46 to said animal, whereby one or more cells of said animal become developmentally competent.

50. A method according to claim 49, wherein said one or more cells are selected from the group consisting of neurons, glial cells, muscle cells, neural cells, and bone marrow cells.

51. A method of identifying one or more molecules that induce developmental incompetence in a cell line, the method comprising:

(a) contacting a developmentally competent cell line with one or more molecules to provide a treated cell line;

(b) separating one or more cells from said treated cell line to provide one or more separated cells;

(c) performing one or more nuclear transfer procedures using each of said separated cells to provide one or more nuclear transfer embryos; and

(d) determining the developmental competence of each of said nuclear transfer embryos by comparing a plurality of nucleic acid molecules obtained from each of said embryos to a gene expression database, whereby said comparison identifies those embryos resulting from nuclear transfer of a developmentally incompetent nuclear donor cell.

52. A method of preventing a full term pregnancy in an animal by inducing developmental incompetence in one or more cells in said animal, the method comprising:

(a) administering one or more molecules identified as inducing developmental incompetence in a cell line by the method of claim 51 to said animal, whereby one or more cells in said animal become developmentally incompetent.

53. A method according to claim 52, wherein said one or more cells are selected from the group consisting of spermatocytes, spermatozoa, oocytes, fertilized oocytes, and embryos.

54. A method of treating a disease in an animal by inhibiting totipotence in one or more cells of the animal, the method comprising:

(a) administering one or more molecules identified as inducing developmental incompetence in a cell line by the method of claim 51 to said animal, whereby one or more cells in said animal become developmentally incompetent.

55. A method of identifying one or more molecules that induce lineage-specific development in a stem cell line, the method comprising:

(a) contacting a stem cell line known to be incapable of differentiation into a specific cell type with one or more molecules to provide a treated cell line;

(b) determining the capability of said treated cell line to differentiate into said specific cell type by comparing a plurality of nucleic acid molecules obtained from said treated cell line to a gene expression database, whereby said comparison identifies stem cells capable of committing to a specific cell lineage.

56. A method of inducing development of a cell into a specific cell type, the method comprising:

(a) contacting a cell with one or more molecules identified as inducing lineage-specific development in a cell line by the method of claim 55, whereby said cell line develops into said specific cell type.

57. A method of treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type, the method comprising:

(a) administering one or more molecules identified as inducing developmental competence in a cell line by the method of claim 55 to said animal, whereby said one or more cells of the animal develop into said specific cell type.

58. A method of identifying one or more molecules that inhibit lineage-specific development in a stem cell line, the method comprising:

(a) contacting a stem cell line known to be capable of differentiation into a specific cell type with one or more molecules to provide a treated cell line;

(b) determining the capability of said treated cell line to differentiate into said specific cell type by comparing a plurality of nucleic acid molecules obtained from said treated cell line to a gene expression database, whereby said comparison identifies stem cells incapable of committing to a specific cell lineage.

59. A method of inhibiting development of a cell into a specific cell type, the method comprising:

(a) contacting a cell with one or more molecules identified as inhibiting lineage-specific development in a cell line by the method of claim 58, whereby said cell line is prevented from developing into said specific cell type.

60. A method of treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type, the method comprising:

(a) administering one or more molecules identified as inducing developmental incompetence in a cell line by the method of claim 59 to said animal, whereby said one or more cells of the animal are prevented from developing into said specific cell type.